EXHIBIT A

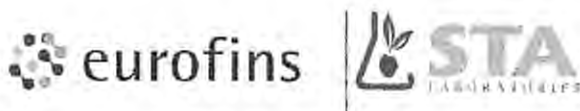**⸭ eurofins** | **STA** LABORATORIES

Data: May 22, 2014

Project Code: DB-8153 (Tomato)

Client: ▓▓▓▓▓▓▓▓▓▓▓▓▓▓▓▓▓▓▓

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Objective: To genotype submitted entries with a set of DNA makers to determine genetic
                  relationships. Specifically, to compare Pomodoro San Marzano variety with other
                  submitted entries.

Entries: Eight (8) samples were received on May 5, 2014 as listed below. ESTA #'s 2 through 8
                  were received as canned whole peel/stewed tomatoes. Seed were extracted from fruit
                  from each entry and dried. Each entry was replicated 2 times and 10 seeds per
                  replication were bulked and used as the source of DNA for screening. This procedure
                  afforded us the opportunity to identity alleles present in 20 plants, which can determine
                  the uniformity of entries and ensure all possible alleles present in a given entry are
                  expressed. (NOTE: A control, ESTA #9 was included to ensure consistent scoring and is
                  a cherry tomato)

ESTA #	Sample Name
1	Pomodoro San Marzano DOP – seed
2	Cento Label 35 oz. ROA 1 L3 M 240
3	Cento Label 28 oz. ROA1 L3 H 247
4	Cento Label 28 oz. ROA 1 L3 H 248
5	Cento Label 28 oz. SL 1 H 231 SM
6	Cento Label 28 oz. SL 1 H 210 SM
7	Cento Label 28 oz. SL 1 M 234 SM
8	Cento Label 28 oz. SL 1 H 217 SM

DNA Markers: Twenty-four (24) primer pairs known as simple sequence repeats (SSR's) were screened
                  with each entry.

Results: Genotypic data were generated following established protocols on an ABI3730XL
                  capillary sequencer and are presented in a three (3) sheet excel workbook, DB-8153
                  Data.xlsx. A summary of each sheet follows:

                  Genotype (9Ex24P: A modified output from the ABI3730XL with entries as rows and
                  SSR markers as columns. Columns A and B rows 2 through 10 lists sample names.
                  Primer designations are in row 1 columns C through Z. Values in respective entry marker
                  cells represent DNA fragment sizes in base pairs. If a single number exist, the respective
                  entry is homozygous for the given locus. If separated by a dash (-) the entry is
                  heterozygous. Different fragment sizes or length polymorphisms among entries for a
                  given marker would indicate that those entries are genetically different. Of the 216
                  possible data points (9 entries x 24 primers), there were 21 missing data points (md).
                  Entry 7 accounted for 11 of those missing data points. Whether the missing data was due
                  to the processing of those tomatoes, i.e. DNA degradation due to heat is unknown at this
                  time. (NOTE: replications were not included as no genotypic differences were detected in
                  the replicated samples)

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Nei&Li (9Ex24P: Nei & Li's dissimilarity genetic distance algorithm is a well accepted method for comparing genetic relationships based on DNA markers. Data is presented in a full rank matrix with all 9 entries. Entry designations are in column A and row 1. Values in respective cells were calculated based on data generated from all 24 primers screened and represent percent genetic dissimilarity rounded to whole numbers. Example; in cell B2 the value is 0 as one is comparing Sample 1 with itself and there is no dissimilarity. (NOTE: genetic similarity=1-dissimilarity).

Dendogram: A tree diagram depicting genetic relationships generated from the data in the fore mentioned page in a graphical format. The numbers on the scale (row **14**) represent percent genetic dissimilarity between entries. Entries that are less dissimilar (more similar) are arranged closer together. Also included in this dendogram are colored blocks indicating SSR results for each entry. If two entries have the same color for a given primer, they represent the same alleles.

Summary: Nine (9) samples were screened with 24 SSR's. Comparing the 7 canned samples with Pomodoro San Marzano none were genetically identical. Genetic similarities ranged from 85% similar to 60% similar. ESTA # 7 (SL 1 H 217 SM) was most similar but that entry did have 11 missing data points thereby using 13 primers in the calculation. What impact these differences have on product quality is unknown.

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